## RECEIVED

<del>ՄՍԼ 0 9 2001</del>

SEQUENCE LISTING

**TECH CENTER 1600/2900** 

BAREILAPA <110> Mahajan, Pramod B. Zuo, Zhuang

<120> Poly ADP-Ribose Polymerase Gene and Its Uses

<130> \( \)718-34, 035718-174234

<140>09\(\chi\_236,995\)

<141> 1999-01-26

<150> 60/072\785

<151> 1998-01**\**27

<160> 5

<170> PatentIn Ver.

<210> 1

<211> 2949

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1)..(2949)

<220>

<221> misc feature

<222> (1)..(2949)

<223> n=A, T, C, or G

<220>

<221> misc feature

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<223> Xaa=unknown

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cgg gcc tcg tgc aag tca tgc cgg tcc cct atc gcc aag gac cag ctc

Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys 🔭 Gln Leu

egt ett gge aag atg gtt eag geg tea eag tte gae gge tte atg eeg 144 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro

atg tgg aac cat gcc agg tgc atc ttc agc aag aag aac cag ata 🗛 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys 50 55

tcc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg gat gat caa

Ser 65	Val	Asp	Asp	Val	Glu 70	Gly	Ile	Asp	Ala	Leu 75	Arg	Trp	Asp	Asp	Gln 80	
					tac Tyr											288
					gag Glu		_					_			-	336
_			_	_	cga Arg	_	_	_	_					_	_	384
					ctt Leu											432
		-		_	ttc Phe 150			_		_		-		-		480
					gat Asp											528
					aaa Lys											576
					agt Ser											624
					aca Thr											672
					ggt Gly 230											720
					agt Ser											768
					gct Ala											816
					gga Gly											864
gat	gga	atg	cta	ttt	gga	gcg	ctg	ggt	cct -2		cca	gtc	tgt	gct	aat	912

Asp	Gly 290	Met	Leu	Phe	Gly	Ala 295	Leu	Gly	Pro	Cys	Pro 300	Val	Cys	Ala	Asn	
														gtg Val		960
														gtt Val 335		1008
														atg Met		1056
					_	_	_							cca Pro		1104
_							_		_					tca Ser	_	1152
_					_	_						-	_	gga Gly		1200
														gct Ala 415		1248
_				_		-	-		_		_	_		att Ile		1296
														agg Arg		1344
-	_				_									gtt Val		1392
_			_	_		-		_					_	tta Leu		1440
														agt Ser 495		1488
														cct Pro		1536
gra	tgg	gaa	aag	cat	ata	caa	tgc	amc	ctt -3		cat	gtt	ctg	acc	tgn	1584



Xaa	Trp	Glu 515	Lys	His	Ile	Gln	Cys 520	Xaa	Leu	Lys	His	Val 525	Leu	Thr	Xaa	
	_							_		_			_	cag Gln	_	1632
														Gly ggg		1680
														gag Glu 575	-	1728
	-	-			_					_				tca Ser		1776
				_						_	-			aga Arg		1824
			-	-	_			_	_		_			cgg Arg		1872
_		_	_	_		_			-			_		gaa Glu		1920
										_	_	_	_	atg Met 655	_	1968
	_			_		-	_				_		_	mag Xaa	_	2016
							_			_		_		tta Leu		2064
														naa Xaa		2112
														atc Ile		2160
														atg Met 735		2208
gaa	gct	ctg	cag	gat	att	gaa	att	gct	tca <b>-4</b>	_	ata	gtt	ggc	ttc	gat	2256

C. A

Glu	Ala	Leu	Gln 740	Asp	Ile	Glu	Ile	Ala 745		Lys	Ile	Val	Gly 750		Asp	
agc Ser	gac Asp	agt Ser 755	Asp	gaa Glu	tct Ser	ctt Leu	gat Asp 760	gat Asp	aaa Lys	tat Tyr	atg Met	aaa Lys 765	ctt Leu	cac	tgt Cys	2304
gac Asp	atc Ile 770	acc Thr	ccg Pro	ctg Leu	gct Ala	cac His 775	gat Asp	agt Ser	gaa Glu	gat Asp	tac Tyr 780	aag Lys	tta Leu	att Ile	gag Glu	2352
cag Gln 785	tat Tyr	ctc Leu	ctc Leu	aac Asn	aca Thr 790	cat His	gct Ala	cct Pro	act Thr	cac His 795	aag Lys	gac Asp	tgg Trp	tcg Ser	ctg Leu 800	2400
gaa Glu	ctg Leu	gag Glu	gaa Glu	gtt Val 805	ttt Phe	tca Ser	ctt Leu	gat Asp	cga Arg 810	gat Asp	gga Gly	gaa Glu	ctt Leu	aat Asn 815	aag Lys	2448
tac Tyr	tca Ser	aga Arg	tat Tyr 820	aaa Lys	aat Asn	aat Asn	ctg Leu	cat His 825	aac Asn	aag Lys	atg Met	cta Leu	tta Leu 830	tgg Trp	cac His	2496
ggt Gly	tca Ser	agg Arg 835	ttg Leu	acg Thr	aat Asn	ttt Phe	gtg Val 840	gga Gly	att Ile	ctt Leu	agt Ser	caa Gln 845	ggg Gly	cta Leu	aga Arg	2544
att Ile	gca Ala 850	cct Pro	cct Pro	gag Glu	gca Ala	cct Pro 855	gtt Val	act Thr	ggc Gly	tat Tyr	atg Met 860	ttc Phe	ggc Gly	aaa Lys	ggc Gly	2592
ctc Leu 865	tac Tyr	ttt Phe	gca Ala	gat Asp	cta Leu 870	gta Val	agc Ser	aag Lys	agc Ser	gca Ala 875	caa Gln	tac Tyr	tgt Cys	tat Tyr	gtg Val 880	2640
gat Asp	agg Arg	aat Asn	aat Asn	cct Pro 885	gta Val	ggt Gly	ttg Leu	atg Met	ctt Leu 890	ctt Leu	tct Ser	gag Glu	gtt Val	gct Ala 895	tta Leu	2688
gga Gly	gac Asp	atg Met	tat Tyr 900	gaa Glu	cta Leu	aag Lys	aaa Lys	gcc Ala 905	acg Thr	tcc Ser	atg Met	gac Asp	aaa Lys 910	cct Pro	cca Pro	2736
aga Arg	ggg Gly	aag Lys 915	cat His	tcg Ser	acc Thr	aag Lys	gga Gly 920	tta Leu	ggc Gly	aaa Lys	acc Thr	gtg Val 925	cca Pro	ctg Leu	gag Glu	2784
tca Ser	gag Glu 930	ttt Phe	gtg Val	aag Lys	tgg Trp	agg Arg 935	gat Asp	gat Asp	gtc Val	gta Val	gtt Val 940	ccc Pro	tgc Cys	ggc Gly	aag Lys	2832
ccg Pro 945	gtg Val	cca Pro	tca Ser	tca Ser	att Ile 950	agg Arg	agc Ser	tct Ser	gaa Glu	ctc Leu 955	atg Met	tac Tyr	aat Asn	gag Glu	tac Tyr 960	2880
atc	gtc	tac	aac	aca	tcc	cag	gtg	aag	atg <b>-5</b> .		ttc	ttg	ctg	aag	gtg	2928

a o

Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val 965 970 975

cgt ttc cat cac aag agg tag Arg Phe His His Lys Arg 980 2949

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<220>
<221> misc\_feature
<222> (1)..(982)
<223> Xaa=unknown

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O out

Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Leu Phe Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu Leu Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu 

and the state of t

Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp 745 Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys 755 760 Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu 775 Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu 790 795 Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys 805 810 Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His 820 825 Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg 840 Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val 870 875 Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu 885 890 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro 900 905 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu 920 925 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Pro Cys Gly Lys 935 940 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr 945 950 955 Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val 970 Arg Phe His His Lys Arg 980

On

<210> 3 <211> 474 <212> DNA <213> Zea mays

<220> <221> CDS <222> (1)..(474)

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aç Se	jc go er Al	ca c .a G 50	aa : ln !	tac Tyr	tg Cy:	t ta s Ty	r va	tg al. 55	gat Asp	age Are	g aa g As	at a	aat Asn	Pr	t gt o Va 0	ta al	ggt Gly	t tt y Le	g eu	atg Met	1	192
	t ct u Le 5	t to u Se	ct ( er (	gag Slu	gt: Va:	T AT	t tt a Le O	a e	gga Gly	gad Asp	c at Me	g t	at Yyr 75	ga Gl	a ct u Le	a eu	aac Lys	g aa S Ly	a 's	gcc Ala 80	2	240
ac Th	g to r Se	c at r Me	g g et <i>P</i>	sp Isp	aaa Lys 85	S PI	t co o Pr	a a	aga Arg	Gl <sup>7</sup>	/ Ly	g c s H O	at	tc Se:	g ac r Th	c ir	aag Lys	gg Gl 9	У	tta Leu	2	88
gg Gl	c aa y Ly	a ac s Th	. v	tg al 00	cca Pro	a ct	g ga ı Gl	g t u S	ca Ser	gag Glu 105	Ph	t g e V	tg	aa Lys	g tg s Tr	p A	agg Arg l10	As	t p	gat Asp	3.	36
gt. Val	c gt. l Va	a gt l Va 11	T 5	cc ro	tgc Cys	ggo Gl	c aa / Ly	S P	cg ro 20	gtg Val	Pro	a to	ca er	tca Ser	a at : Il 12	e A	agg Arg	ago Sei	c r	tct Ser	38	84
gaa Glu	a cto 1 Leu 130	1 110	g t t T	ac yr	aat Asn	gaç	ta Ty: 13	r 1	tc le	gtc Val	tac Tyr	c aa	ac sn	aca Thr 140	Se	c c	ag Iln	gto Val	g a L :	aag Lys	43	32
ato Met 145	g cag Glr	tt. Ph	c t: e Le	tg eu :	ctg Leu	aag Lys 150	۷a.	g c	gt rg	ttc Phe	cat His	: ca Hi 15	İs	aag Lys	ago	g t	ag				47	74
<21 <21	0> 4 1> 1 2> P 3> Z	57 RT	nays	3																		
<40	0> 4																					
Asn 1	Lys				J						10							1 5				
iie	Leu	Ser	· G1 2	n (	Sly	Leu	Arg	Il	.e <i>1</i>	Ala 25	Pro	Pr	0 (	Slu	Ala			Val	T	hr		
Gly	Tyr	Met 35	Ph	e G	Sly	Lys	Gly	Le 4	u 1	yr	Phe	Al	a P	qz		Vá	30 al	Ser	L	ys		
Ser	Ala 50	Gln	Ту	r C	ys	Tyr	Val 55	As	p F	Arg .	Asn	Ası	n F	ro	45 Val	G1	.у	Leu	M	et		
Leu 65	Leu	Ser	Gl	u V	al	Ala 70	Leu	Gl	уА	sp i	Met	Тy	r G	60 Slu	Leu	Ly	s :	Lys	A.	la		
	Ser	Met	As	p L	ys		Pro	Ar	g G	ly :	Lys	7: His	s S	er	Thr	Ly	s (	Gly	Le	80 eu		
	Lys		Va.	l P	0.0				r G	lu 1	90							OΕ				
	Val	Val	ΤΟ.	J				Pr	0 V	05						7 7	Λ.					
	Leu 130	110											ı T	hr	1つに							
Met 145	Gln	Phe	Let	1 L	eu 1	Lys 150	Val	Ar	g P	he H	lis	His	L	40 ys	Arg							

Cul

<210> 5 <211> 530 <212> DNA <213> Zea mays

Con Contraction

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